

Amendment to the claims:

This listing of claims will replace all prior versions, and listing, of claims in the application:

1. **(Currently amended)** A method for determining if a soybean has Rps8-derived *Phytophthora sojae* resistance ~~the presence of trait locus Rps8 in a soybean wherein the presence of trait locus Rps8 confers resistance to *Phytophthora sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7 and combinations thereof~~, comprising:

(a) analyzing genomic DNA from the soybean for the presence of a combination of molecular markers on major linkage group F which are associated with ~~said~~ trait locus Rps8, whereby detecting the presence of the molecular markers provides an indication that said ~~trait locus Rps8-derived *P. sojae* resistance~~ is present in the soybean; and

(b) confirming that the soybean has Rps8-derived *P. sojae* resistance by inoculating the soybean with one or a combination of *P. sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6 or 7 to which the soybean would be susceptible if the soybean did not have Rps8-derived *P. sojae* resistance;

wherein Rps8-derived *P. sojae* resistance confers resistance to all *P. sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6 and 7.

2. **(Previously presented)** The method of claim 1 wherein the molecular markers are selected from the group consisting of Satt516, Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

3. **(Currently amended)** The method of claim 1 wherein the molecular markers are markers Satt516 and Satt114 ~~and wherein the method further comprises a step of determining that the soybean does not contain trait locus Rps3.~~

4. **(Withdrawn)** A method for introgressing soybean *Phytophthora sojae* resistance into non-resistant soybean germplasm or less resistant soybean germplasm comprising:

providing a first soybean germplasm which has Rps8-derived resistance to *Phytophthora sojae* and which has been selected by marker assisted selection using one or more nucleic acid markers, wherein the soybean *Phytophthora sojae* resistance is associated with the Rps8 gene that maps to soybean major linkage group F and wherein the molecular markers are associated with the Rps8 gene;

providing a second soybean germplasm which lacks Rps8-derived resistance to *Phytophthora sojae*;

crossing the first soybean germplasm with the second soybean germplasm to introgress the Rps8 gene into the genome of the second soybean germplasm to provide a hybrid introgressed germplasm having Rps8-derived resistance to *Phytophthora sojae*.

5. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is HFX01-602, or a descendant thereof.

6. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is OX-99128, or a descendant thereof.

7. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is OX-98317, or a descendant thereof.

8. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is selected by a marker assisted selection technique selected from the group consisting of SSR analysis, RFLP analysis, RAPD analysis, and isozyme analysis.

9. **(Withdrawn)** The method of claim 4 wherein the nucleic acid markers are selected from the group consisting of. Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

10. **(Withdrawn)** A method for the production of a soybean cultivar adapted for conferring, in hybrid combination with a suitable second inbred, resistance to *Phytophthora sojae* comprising:

selecting a first donor parental line possessing the desired *Phytophthora sojae* resistance said first donor parental line comprising a *Phytophthora sojae* resistance gene Rps8 which is located on major linkage group F; crossing the first donor parental line with a second parental line, which is high yielding in hybrid combination, to produce a segregating plant population of genetically heterogeneous plants;

screening the plants of the segregating plant population for the gene Rps8 by marker assisted selection using at least one associated markers;

selecting plants from the population having the gene Rps8; and

breeding by self crossing the plants containing the Rps8 gene until a line is obtained which is homozygous for resistance to *Phytophthora sojae* at Rps8 to give resistance to *Phytophthora sojae*.

11. **(Withdrawn)** The method of claim 10 wherein the at least one associated marker is selected from the group consisting of. Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

12. **(Withdrawn)** The method of claim 10 wherein the molecular markers are Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

13. **(Withdrawn)** The method of claim 10 wherein the first donor parental line is HFX01-602, or a descendant thereof.
14. **(Withdrawn)** The method of claim 10 wherein the first donor parental line is OX-99128, or a descendant thereof.
15. **(Withdrawn)** The method of claim 10 wherein the first donor parental line is OX-98317, or a descendant thereof.
16. **(Withdrawn)** The method of claim 10 wherein the plants of the segregating plant population are screened by a marker assisted selection technique selected the marker assisted selection comprises analyzing by a technique selected from the group consisting of, SSR analysis,.
17. **(Withdrawn)** A method for reliably and predictably introgressing soybean Rps8-derived resistance to *Phytophthora sojae* into susceptible soybean germplasm comprising analyzing soybean germplasm lines by marker assisted selection to identify those soybean germplasm lines having the Rps8 gene; and introgressing said Rps8 gene into said non-resistant soybean germplasm.
18. **(Withdrawn)** The method of claim 18 wherein markers for use in marker assisted selection are selected from the group consisting of. Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.
19. **(Withdrawn)** The method of claim 18 wherein the marker assisted selection comprises the use of SSR analysis.
20. **(Withdrawn)** A soybean plant produced according to the method of any one of claims 1-22.

21. **(Withdrawn)** A soybean plant having resistance to *Phytophthora sojae* comprising:

a soybean germplasm comprising an Rps8 gene
wherein the germplasm was produced by introgression of a soybean germplasm containing Rps8 in its genome with a soybean germplasm lacking the Rps8 gene in its genome.

22-24. **(Cancelled)**

25. **(Currently amended)** The method of claim 1, wherein the soybean is a progeny resulting from a cross between two parents wherein at least one parent has Rps8-derived *Phytophthora P. sojae* resistance and wherein said parent is identified by inoculation with one or more *P. sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7 or combinations thereof.

26. **(Currently amended)** The method of claim 25, wherein the at least one parent that has Rps8-derived *Phytophthora P. sojae* resistance is a soybean of plant line PI 399073 or a descendant thereof.

27. **(Currently amended)** A method of selecting a soybean plant having ~~trait locus~~ Rps8-derived *Phytophthora sojae* resistance, comprising:

(a) ~~selecting~~ providing a soybean plant that is a progeny from a cross between a first parent that has Rps8-derived *Phytophthora P. sojae* resistance and a second parent that does not have Rps8-derived *Phytophthora P. sojae* resistance;

(b) detecting in the first parent a first nucleic acid ~~from the first parent~~ which is genetically linked to trait locus Rps8, wherein trait locus Rps8 is mapped to a locus on major linkage group F that is located between molecular markers Satt114 and Satt516; and

(c) ~~selecting~~ identifying a soybean plant as having trait locus Rps8 by screening the soybean plant progeny comprising for the presence of the first nucleic acid thereby selecting the soybean plant having trait locus Rps8;

(d) inoculating the soybean plant identified as having trait locus Rps8 with one or a combination of *P. sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6 or 7 to which the soybean plant would otherwise be susceptible if the soybean plant did not have Rps8-derived *P. sojae* resistance to confirm that the soybean plant has Rps8-derived *P. sojae* resistance;

wherein Rps8-derived *P. sojae* resistance confers resistance to all *P. sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6 and 7; and,

(e) selecting the soybean plant that has been identified as having the Rps8 trait locus and that has been confirmed as having Rps8-derived *P. sojae* resistance.

28. **(Previously presented)** The method of claim 27, wherein the first nucleic acid is a marker selected from the group consisting of:

(a) Satt 114, Satt 516, Satt595, Satt334, Sat_317, Sat_197, Satt510, Satt335, Satt144; and

(b) a marker linked to a marker of (a).

29. **(Previously presented)** The method of claim 27, wherein detecting the first nucleic acid comprises microsatellite analysis.

30. **(Previously presented)** The method of claim 27, wherein detecting the first nucleic acid comprises hybridization of a second nucleic acid to the first nucleic acid.

31. **(Previously presented)** The method of claim 27, wherein the first parent is a soybean of plant line PI 399073 or a descendant thereof.

32. **(Currently amended)** The method of claim 27, wherein ~~trait locus~~ Rps8-derived resistance is derived from the plant line HFX01-602 or a descendant thereof.

33. **(Currently amended)** A method of identifying soybean plants that are likely to have trait locus Rps8, the method comprising:

(a) detecting a first locus on the genome of the plant which is genetically linked to trait locus Rps8, wherein the first locus maps to major linkage group F and is located between molecular marker Satt114 and Satt516; and

(b) determining that the soybean plant does not have Rps3.

~~whereby detecting the first locus in the plant provides an indication that the trait locus Rps8 is present in the plant.~~

34. **(Previously presented)** The method of claim 33, wherein the first locus is linked to a marker selected from the group consisting of Satt595, Satt334, Sat_317, Sat_197, Satt510, Satt335, and Satt144.

35. **(Currently amended)** A method of selecting a soybean plant having Rps8-derived *Phytophthora sojae* resistance, comprising:

(a) producing a progeny from a cross between a first parent that has Rps8-derived ~~*Phytophthora-P. sojae*~~ resistance and a second parent that does not have Rps8-derived ~~*Phytophthora-P. sojae*~~ resistance;

(b) detecting a ~~*Phytophthora-P. sojae*~~ isolate that the second parent is susceptible to, wherein said ~~*Phytophthora-P. sojae*~~ isolate is selected from the group consisting of pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, and combinations thereof; and

(c) selecting the progeny that is resistant to said ~~*Phytophthora-P. sojae*~~ isolate, thereby selecting a soybean plant having Rps8- derived ~~*Phytophthora-P. sojae*~~ resistance.

36. **(Currently amended)** The method of claim 35, wherein the ~~*Phytophthora*~~*P.* *sojae* isolate is selected from the group consisting of *P. sojae* race 1, race 4, race 17, race 25, race 30, and combinations thereof.

37. **(Currently amended)** The method of claim 35, wherein ~~that~~ the first parent is a plant variety selected from the group consisting of HFX01-602, OX-98317, OX-99218, OX-99128 or descendants thereof.

38. **(Previously presented)** The method of claim 27, wherein the first parent is a plant variety selected from the group consisting of OX-98317, OX-99218, OX-99128 or descendants thereof.

39. **(Currently amended)** The method of claim 27, wherein the Rps8 derived ~~*Phytophthora*~~*P.* *sojae* resistance of the first parent is determined by inoculation of the first parent with one or more *P. sojae* pathotypes selected from the group consisting of pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, and combinations thereof.

40. **(Currently amended)** The method of claim 25, wherein the at least one parent that has Rps8 derived ~~*Phytophthora*~~*P.* *sojae* resistance is a plant variety selected from the group consisting of HFX01-602, OX-98317, OX-99218, OX-99128 or descendants thereof.

41. **(Withdrawn)** A trait locus Rps8, wherein said trait locus Rps8 confers soybean resistance to *Phytophthora sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, and all combinations thereof, and wherein said trait locus maps to a region of soybean major linkage group F that is flanked by molecular marker Satt516 and a molecular marker selected from the group consisting of Satt114, Satt334, Sat_317, Satt335, Satt510, Satt144 and Sat_197.

42. **(New)** The method of claim 1, wherein step b comprises selecting for inoculation of the soybean a *P. sojae* isolate to which a parent of the soybean that lacks Rps8-derived *P.*

sojae resistance is susceptible and inoculating the soybean with said isolate to confirm that the soybean has Rps8-derived *P. sojae* resistance.

43. **(New)** The method of claim 1, wherein step b comprises inoculating the soybean with a *P. sojae* pathotype that has virulence to Rps3a, Rps3b, or Rps3c, but not Rps8.

44. **(New)** The method of claim 1, wherein step b comprises inoculating the soybean with *P. sojae* race 7 or 17.

45. **(New)** The method of claim 1, comprising the step of determining that the soybean is a progeny from parents that lack Rps3.

46. **(New)** The method of claim 27, wherein step d comprises inoculating the soybean having trait locus Rps8 with a *P. sojae* isolate to which a parent of the soybean is susceptible.

47. **(New)** The method of claim 27, wherein step d comprises inoculating the soybean having trait locus Rps8 with a *P. sojae* pathotype that has virulence to Rps3a, Rps3b, or Rps3c, but not Rps8.

48. **(New)** The method of claim 27, wherein step d comprises inoculating the soybean having trait locus Rps8 with *P. sojae* race 7 or 17.

49. **(New)** The method of claim 27, comprising the step of determining that the soybean is a progeny from parents that lack Rps3.

50. **(New)** The method of claim 33, wherein step b comprises inoculating the soybean with a *P. sojae* pathotype that has virulence to Rps3a, Rps3b, or Rps3c, but not Rps8.

51. **(New)** The method of claim 33, wherein step b comprises inoculating the soybean with *P. sojae* race 7 or 17.

52. **(New)** The method of claim 33, wherein step b comprises determining that the soybean is a progeny from parents that lack Rps3.